

AMENDMENTS TO THE SPECIFICATION:

Please replace the paragraph beginning on line 31 of page 22, and ending with line 14 of page 23 with the following amended paragraph:

The determination of percent homology (i.e. percent identity) described herein between two amino acid or nucleotide sequences can be accomplished using a mathematical algorithm. For example, a mathematical algorithm useful for comparing two sequences is the algorithm of Karlin and Altschul (1990, Proc. Natl. Acad. Sci. USA 87:2264-2268), modified as in Karlin and Altschul (1993, Proc. Natl. Acad. Sci. USA 90:5873-5877). This algorithm is incorporated into the NBLAST and XBLAST programs of Altschul, et al. (1990, J. Mol. Biol. 215:403-410), and can be accessed, for example, at the National Center for Biotechnology Information (NCBI) world wide web site having the universal resource locator "~~<http://www.ncbi.nlm.nih.gov/BLAST/>~~" "www.ncbi.nlm.nih.gov/BLAST". Blast nucleotide searches can be performed with NBLAST program (designated "blastn" at NCBI web site), using the following parameters: gap penalty = 5; gap extension penalty = 2; mismatch penalty = 3; match reward = 1; expectation value 10.0; and word size = 11 to obtain nucleotide sequences homologous to a nucleic acid described herein. BLAST protein searches can be performed with XBLAST program (designated "blastn" at the NCBI web site) or the NCBI "blastp" program, using the following parameters: expectation value 10.0, BLOSUM62 scoring matrix to obtain amino acid sequences homologous to a protein molecule described herein.

Please replace the paragraph beginning on line 15 of page 23 with the following amended paragraph:

To obtain gapped alignments for comparison purposes, Gapped BLAST can be utilized as described in Altschul et al. (1997, Nucleic Acids Res. 25:3389-3402).

Alternatively, PSI-Blast or PHI-Blast can be used to perform an iterated search which detects distant relationships between molecules (id.) and relationships between molecules which share a common pattern. When utilizing BLAST, Gapped Blast, PSI-Blast, and PHI-Blast programs, the default parameters of the respective programs (e.g., XBLAST and NBLAST) can be used. See <http://www.ncbi.nlm.nih.gov> the world wide web having the universal locator www.ncbi.nlm.nih.gov.

Please replace the paragraph beginning on line 10 of page 56 with the following amended paragraph:

Under the terms of the Budapest Treaty on the International Recognition of the Deposit of Microorganisms for the Purpose of Patent Procedure, ~~deposit of a hybridoma, KKO~~ deposit of hybridoma KKO ~~will be~~ was made on July 30, 2004 with the American Type Culture Collection (ATCC) of 10801 University Blvd., Manassas, Virginia, 20110-2209 USA, and given ATCC patent deposit designation number PTA-6133. ~~where the deposits are given ATCC Accession Numbers _____.~~ The assignee, Science & Technology Corporation @ UNM, represents that the ATCC is a depository afforded permanence of the deposit and ready accessibility thereto by the public if a patent is granted. All restrictions on the availability to the public of the material so deposited will be irrevocably removed upon granting of a patent. The material will be readily available during the pendency of the patent application to one determined by the Commissioner to be entitled thereto under 37 C.F.R. §1.14 and 35 U.S.C. §122. The deposited material will be maintained with all the care necessary to keep it viable and uncontaminated for a

after the most recent request for the furnishing of a sample of the deposited material, and in any case, for a period of at least thirty (30) years after the date of the deposit or for the enforceable life of the patent, whichever period is longer. Applicant's assignee acknowledges its duty to replace the deposit should the depository be unable to furnish a sample when requested due to the condition of the deposit.